

# The important role of evolution in the Planck $Y_{SZ}$ –mass calibration

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## ABSTRACT

In light of the tension between cosmological parameters from Planck cosmic microwave background and galaxy clusters, we revised the Planck analysis of the  $Y_{SZ}$ –mass calibration to allow evolution to be determined by the data instead of being imposed as an external constraint. Our analysis uses the very same data and Malmquist bias corrections as used by the Planck team in order to emphasize that differences in the results come from differences in the assumptions. The evolution derived from 71 calibrating clusters, with  $0.05 < z < 0.45$ , is proportional to  $E^{2.5 \pm 0.4}(z)$ , so inconsistent with the self-similar evolution ( $E^{2/3}$ ) assumed by previous analyses. When allowing for evolution, the slope of  $Y_{SZ}$ –mass relation turns out to be  $1.51 \pm 0.07$ , which is shallower by  $4.8\sigma$  than the value derived when assuming self-similar evolution, introducing a mass-dependent bias. The non-self-similar evolution of  $Y_{SZ}$  has to be accounted for in analyses aimed to establish the biases of Planck masses.

**Key words.** Galaxies: clusters: general — Methods: statistical — Cosmology: observations — Galaxies: clusters: intracluster medium

## 1. Introduction

The Sunyaev-Zel’dovich (SZ) effect, which is the distortion caused by the high energy electrons of the intracluster medium on the cosmic microwave background (CMB) photons, has been used by Ade et al. (2014a) to put constraints on cosmological parameters using Planck data. The cosmological constraint comes from matching the galaxy cluster abundance (per unit observable) to the cluster mass function (per unit mass), via a mass–observable relation. At present, the Planck mass–observable calibration is a two–step process (Ade et al. 2014a,b): first, the  $Y_X$  mass proxy ( $Y_X = T_X M_{gas}$ , Kravtsov et al. 2006) is calibrated against hydrostatic masses (Arnaud et al. 2010), and, second, this calibration is transferred to the  $Y_{SZ}$  proxy using the measured  $Y_{SZ}$  values for 71 clusters (with  $Y_X$  values) observed by Planck (Ade et al. 2014a,b). This calibration uses clusters spread over a sizeable redshift range ( $0 < z < 0.5$ , see Fig. 1) and assumes a given (self-similar) evolution for the mass proxies. The assumption of a self-similar evolution relies on the the self-similar model (Kaiser 1991) and numerical simulations (Kravtsov et al. 2006) and lacks an observational determination, i.e. a calibration done using directly measured masses (i.e. weak lensing) at various redshifts.

The cosmological constraints derived by Planck using galaxy clusters differ from those derived (mostly) from the CMB (Ade et al. 2014a). In particular, the best fit CMB cosmology predicts many more clusters than observed, suggesting that the current Planck-estimated masses may be underestimated.

Rozo et al. (2012) use Chandra data from Vikhlinin et al. (2009) and a subsample of an early Planck sample (Ade et al. 2011) to argue that the calibration may have an intercept and, possibly, a slope, lower than derived in Ade et al. (2011), which uses the same  $Y_{SZ}$  values but  $Y_X$  values derived from XMM data. The lower intercept agrees with X–ray expectations (Rozo et al. 2012). Rozo et al. (2012) also find no evidence of any evolution in the intercept of the  $Y_{SZ} - Y_X$  relation, giving indirect support to the self-similar evolution assumed by the Planck team but under

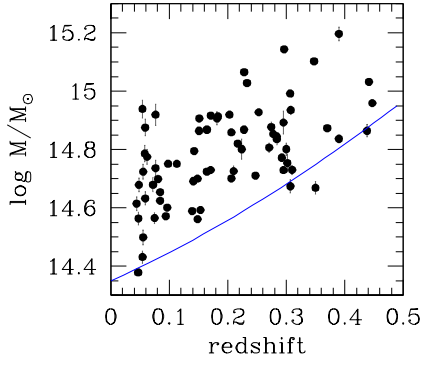
a number of restrictive hypothesis. For example, they hold fixed the slope of the relation and they suppose to perfectly know the evolution of  $Y_X$ .

Recently, von der Linden et al. (2014) have compared Planck SZ mass estimates to weak-lensing masses and found that Planck masses need to be underestimated at a  $\sim 1.6\sigma$  level and, with modest evidence, need it even more so with increasing masses. Similar clues have also been found by Sereno et al. (2014) for the von der Linden et al. (2014) sample and for other samples as well. Analyses of these two works assume a self-similar evolution and therefore attribute the tilted scaling to a mass bias. However, Andreon & Congdon (2014) and Gruen et al. (2014) note that the mass slope and the evolution of the scaling may be collinear (degenerate)<sup>1</sup>. Therefore, the claimed mass bias can be a manifestation of an evolution in the  $Y_{SZ}$ –mass scaling.

Because the evolution of  $Y_{SZ}$  is unlikely to be perfectly known and because there are hints in the literature of possible mass-dependent biases that could instead be manifestations of redshift effects, in this paper we independent assess the Planck mass calibration. Our approach is free of evolutionary assumptions and breaks the mass–redshift degeneracy. More specifically, we fit the  $Y_{SZ}$ –mass allowing (solving for) evolutionary effects that have been neglected in the previous mass calibration. If ignored, these effects lead to a mass-dependent bias. In particular, we use the very same input data as used by the Planck team, in order to emphasize that differences in the results come from differences in the assumptions.

We assume  $\Omega_M = 0.3$ ,  $\Omega_\Lambda = 0.7$ , and  $H_0 = 70 \text{ km s}^{-1} \text{ Mpc}^{-1}$ . Results of stochastic computations are given in the form  $x \pm y$  where  $x$  and  $y$  are the posterior mean and standard deviation. The latter also corresponds to 68 % intervals, because we only summarized posteriors close to a Gaussian in that way. All log are in base 10.

<sup>1</sup> Sereno et al. (2014) also mention this possibility, but their analysis does not account for it.



**Fig. 1.** Mass vs redshift plot of the Planck calibrating sample. Points are  $M_{500}^{YX}$  masses. The solid line marks the adopted threshold mass  $M_{thr}$  of our secondary analysis (sec. 2.1).

## 2. Revisiting the $Y_{SZ}$ calibration

Our starting point is the catalogue of the  $Y_X$ -derived masses,  $M_{500}^{YX}$ , and Malmquist-bias-corrected  $Y_{SZ}$  values delivered by the Planck team for the 71 calibrating clusters<sup>2</sup>. Their calibration sample has an increasing limiting mass with redshift (Fig. 1).

Following Ade et al. (2014a,b), we fit the data with the function

$$\log Y_{SZ,z} = \log Y_{SZ,z=0} + \gamma \log E(z) + s(\log(M_{500}^{YX}/M_{ref})) \quad (1)$$

allowing a log-normal scatter in  $Y_{SZ}|M_{500}^{YX}$  around the mean relation, where  $M_{ref} = 6 \cdot 10^{14} M_{\odot}$ . In contrast to Ade et al. (2014a,b), we leave the  $\gamma$  parameter free, rather than freezing it to the self-similar value (2/3). This is an important difference, because we no longer assume the self-similar evolution, and we are trying to solve for the  $Y_{SZ}$ -mass scaling *and* its evolution. The fit is performed using the standard errors-in-variables Bayesian regression (Dellaportas & Stephens, 1995; see Andreon & Hurn 2013 for an introduction)<sup>3</sup>.

The mass- $Y_{SZ}$ -redshift fit results are shown in Fig. 2. We found that  $\log Y_{SZ}$  scales with  $\log M_{500}^{YX}$  with slope  $s = 1.51 \pm 0.07$ , with a negligible intrinsic scatter ( $\log Y_{SZ}|M_{500}^{YX} = 0.06 \pm 0.01$  dex),

$$\log Y_{SZ,z} = (1.51 \pm 0.07)(\log(M_{500}^{YX}/M_{ref})) - 4.26 \pm 0.02 + (2.5 \pm 0.4) \log E(z) \quad (2)$$

with some covariance between the mass slope  $s$  and the evolutionary term  $\gamma$ , as shown in Fig. 3. The evolution of the  $Y_{SZ}$ -mass scaling is well constrained by the data,  $\gamma = 2.5 \pm 0.4$ , mainly because a sizeable range of masses are available at a given redshift (because of the vertical spread at a fixed  $z$  in Fig. 1). Indeed, if the relation in Fig. 1 were scatterless, then a complete collinearity (degeneracy) between the  $Y_{SZ}$ -mass slope and the redshift evolution would be present, meaning the slope evolution could not be measured without assuming a slope for the relation. The scatter breaks the collinearity. This is not the case for the Gruen et al. (2014) sample, formed by just seven clusters, as also noted by the authors.

The evolutionary term  $\gamma$  derived from the data,  $\gamma = 2.5 \pm 0.4$ , is much larger than the self-similar value assumed in the Ade et al. (2014a,b) fitting,  $\gamma = 2/3$ . Indeed,  $\gamma = 2/3$  is rejected by the

data because the posterior probability of  $\gamma = 2/3$  is extremely low (i.e. more than  $> 500$  times smaller than the modal value). Furthermore,  $\gamma = 2/3$  is just outside the boundary of the 99.9 % interval of  $\gamma$  (Fig. 3), and only 0.01% of the Monte Carlo samples have lower  $\gamma$ . Expressed in another way, the  $\gamma$  value derived from the data differs from the one assumed in the Ade et al. (2014a,b) fit in a way that makes the new and old mass slopes different by 4.8 times the slope error quoted in Ade et al. (2014a,b). The disagreement between the evolution pointed out by the data and the one assumed in previous works (e.g. Rozo et al. 2012, Sereno et al. 2014, von der Linden et al. 2014, Ade et al. 2014a,b) is also illustrated in the right-hand panel of Fig. 2:  $Y_{SZ}$  residuals (i.e. observed minus fitted) have a slope of  $\sim 2.5$  (solid line), not 2/3 (dotted line).

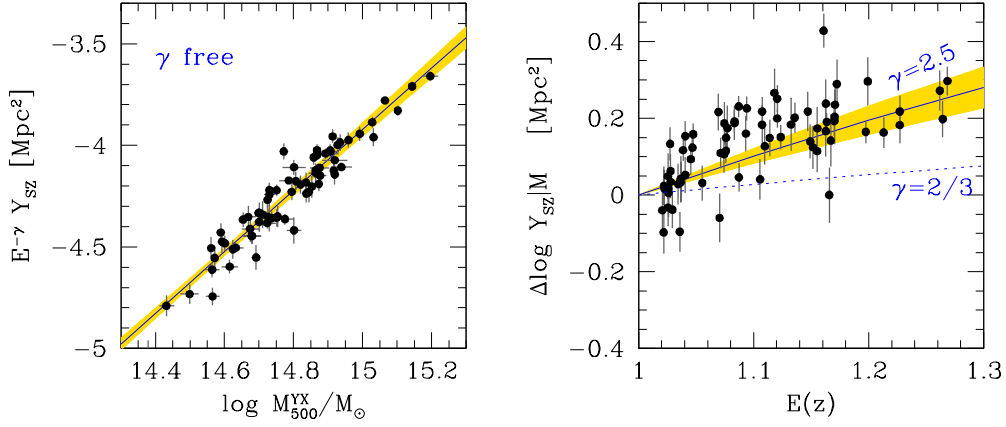
Equation 3 has an immediate consequence: the mass slope of quantities like  $E^{-2/3} Y_{SZ}$  or any quantity built from it like Planck masses, depends on how the studied clusters are distributed in the mass-redshift plane. If clusters are all at the same redshift, then the correct slope is recovered (because in such a case  $E(z)$  is a constant), but if the mass distribution changes with redshift (e.g. because of selection effects), a biased slope is found because of the mismatch between the true data dependency,  $E^{2.5}$ , and the assumed evolution,  $E^{2/3}$ . The sample used in the  $Y_{SZ}$ -mass analysis of Rozo et al. (2012) has a very narrow redshift distribution: 70% of their sample is at  $0.04 < z < 0.10$ . Their slope is, therefore, unaffected by holding the evolutionary term fixed to  $E^{2/3}$ . Instead, the samples used in the  $Y_{SZ}$ -mass analyses in von der Linden et al. (2014) and Sereno et al. (2014) are distributed over a sizeable redshift range. For these studies it still needs to be evaluated whether the effect interpreted as a mass bias is instead a consequence of the assumption of a self-similar evolution.

In Figure 4, we show the ratio between the recalibrated and original masses for the whole Planck cosmological sample and for two redshift subsamples. At a fixed redshift, points are aligned on a line of slope 0.28 (the difference in slope between the two calibrations), introducing a mass-dependent bias. The intercept decreases with increasing redshift or, equivalently, the abscissa (mass) at which the two calibrations equal each other increases with redshift. At a fixed redshift, the most massive clusters tend to have recalibrated masses five to ten percent higher than originally quoted (Figure 4), in the same direction as suggested by von der Linden et al. (2014) and Sereno et al. (2014), by analyses that assume, however, a self-similar evolution. Instead, the originally derived Planck masses are biased high at the lowest masses entering in the cosmological sample (Figure 4). Therefore, at face value, our new calibration implies more clusters than the original calibration, which already produces more clusters than observed for the Planck CMB cosmology. In other terms, the recalibration does not seem to solve the tension between the CMB- and cluster-based cosmologies. Nevertheless, we want to emphasize that  $Y_{SZ}$  proxy values of the cosmological sample are derived by the Planck team when assuming their  $Y_{SZ}$ -mass scaling, not ours. Therefore our conclusion about the role of evolution in solving the tension between the CMB- and cluster-based cosmologies should be re-evaluated after consistently deriving  $Y_{SZ}$  proxy values with the updated calibration (i.e. with eq. 2). A re-extraction of the  $Y_{SZ}$  values of the Planck cluster catalogue is beyond the scope of this work.

Finally, we would like to emphasize that the current Planck calibration is indirect because it is based on the mass surrogate  $Y_X$ , assumed to be self-similar evolving. Therefore, the found non-self-similar evolution of the  $Y_{SZ}$ -mass calibration can be

<sup>2</sup> The table is available at <http://szcluster-db.ias.u-psud.fr>.

<sup>3</sup> The fitting code is available at <http://www.brera.mi.astro.it/~andreon/fitSZplanck.bug>.



**Fig. 2.** Mass- $Y_{SZ}$  scaling (left-hand panel) and residuals (observed minus expected) as a function of redshift (right-hand panel). The solid line marks the mean fitted regression line. The shaded region marks the 68% uncertainty (highest posterior density interval) for the regression. In the left-hand panel, measurements are corrected for evolution. In the right-hand panel the dotted line shows the  $E^{2/3}$  dependency assumed by the Planck team.

genuine, i.e. related to a non-self-similar evolution of the SZ mass proxy itself, or induced by a possible non-self-similar evolution of the mass surrogate  $Y_X$ . In fact, the evolution of the  $Y_X$ -mass scaling lacks an observational determination, since our current knowledge is currently limited to a consistency check (Israel et al. 2014), at the differences of the richness, that has a directly measured (non-) evolution (Andreon & Congdon, 2014).

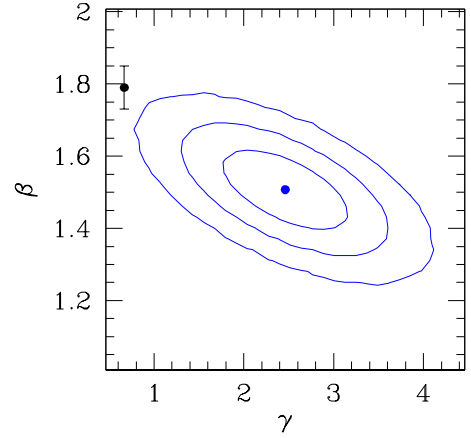
### 2.1. Alternative treatment of the mass and selection function

We now show that the precise schema used to correct for the sample selection function and for the Malmquist bias has little practical consequences. To correct for the Malmquist bias, we now take the non-Malmquist bias-corrected data and compute the mass function and its evolution from the Multidark simulation (Prada et al. 2012; the data are available in CosmoSim, Riebe et al. 2013). We assume that the selection function is a step function with a threshold mass,  $M_{thr}$ , linearly increasing with  $E(z)$ :

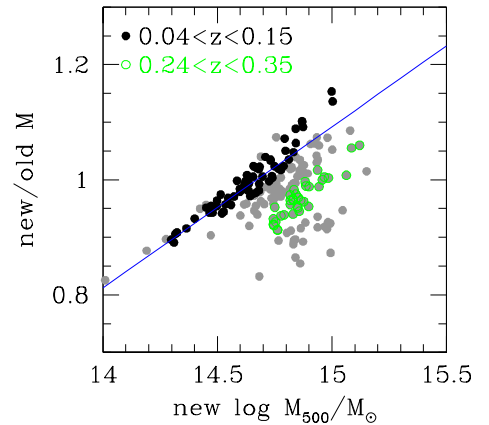
$$\log M_{thr} = 2 (E(z) - 1.1) + 14.55 \quad (3)$$

as shown in Fig. 1. This approach properly deals with the Malmquist bias as a stochastic (variable for clusters of the same observed mass) and uncertain correction instead of a deterministic and perfectly known constant according to the Planck and our baseline analyses<sup>4</sup>. We found  $s = 1.50 \pm 0.07$  (vs  $s = 1.51 \pm 0.07$  in the baseline analysis) and  $2.1 \pm 0.4$  (vs  $\gamma = 2.4 \pm 0.5$ ). The value  $\gamma = 2/3$  is rejected at 99.9 %, showing that our results are robust to the precise treatment of the mass+selection function.

<sup>4</sup> The code used for the fitting is, after minor editing, the same Bayesian code as described in and distributed by Andreon & Bergé (2012), and used in Andreon & Condon (2014) for analysing the determination of the evolution of the richness-mass scaling. We assume weak priors on slope, intercept, and intrinsic scatter and solve for all variables at once. We account, as mentioned, for the scatter, evolution, mass, and selection function. We used a computationally inexpensive 10 million long MCMC chain, discarding the initial 10 thousand elements used for burn-in. By running multiple chains, we checked that convergence is already achieved with short chains.



**Fig. 3.** Bounds on the mass slope  $s$  and evolutionary parameter  $\gamma$  of the  $Y_{SZ}$ -mass relation (68, 95, 99.7%, from inner to outer contours). The point with error bar marks the slope derived in Ade et al. (2014) for the assumed  $\gamma = 2/3$ .



**Fig. 4.** Ratio between the recalibrated and original mass from Planck  $Y_{SZ}$  for the cosmological Planck sample (gray background) and for two redshift subsamples (black closed points and green open points). The blue line has a slope equal to 0.28.

### 3. Summary

We refitted the values of the 71 Planck clusters in the Planck calibration sample by allowing evolution to be determined from the data, i.e. letting the power of the  $E(z)$  term be free, instead of fixed to  $2/3$ . We used the very same input numbers as the Planck team in order to emphasize that differences in the results come from differences in the assumptions. We also repeated the analysis twice, once adopting the Planck team corrections for Malmquist bias and once directly dealing with the mass and selection function. The two analyses consistently found (eq. 2) a shallower  $Y_{SZ}$ -mass relation with a stronger evolution than assumed by the Planck team, i.e. a mass-dependent bias. The assumed (by the Planck team) self-similar evolution, i.e.  $\gamma = 2/3$ , is rejected at  $\geq 99.9\%$  confidence by their own fitted data, which instead favour an  $E^{2.5 \pm 0.4}(z)$  evolution. This suggests caution in interpreting results of works that assume a self-similar evolution and determine, or revisit, the Planck proxy-mass calibration under such an assumption because what is said to be a mass bias could be a neglected evolutionary term.

Our revised calibration is, at first sight, not useful for reducing the tension between the CMB- and cluster-based cosmologies because at face value it increases, instead of reducing, the already too large number of expected clusters for the Planck CMB cosmology. However, this conclusion should be re-evaluated after rederiving  $Y_{SZ}$  proxy values of the cosmological sample with a proxy-mass relation with an evolution consistent with the data (i.e. with eq. 2).

The bottom line is that the non-self-similar evolution of the SZ proxy cannot be ignored:  $\gamma = 2.5$  (supported by the data) has to be preferred to  $\gamma = 2/3$  (self-similar). Waiting for a re-derivation of the  $Y_{SZ}$  values, we suggest estimating the masses for Planck clusters using our eq. 2 and the  $Y_{SZ}$  values listed in the Planck catalogue.

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